

SEQUENCE LISTING

<110> Hayward, Nicholas K.
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<120> A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
SAME

<130> DAVIES

<140> 08/765,588

<141> 1996-02-22

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 649

<212> DNA

<213> Nucleotide Sequence of VEGF165

<220>

<221> CDS

<222> (17)..(589)

<400> 1
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Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
1 5 10

gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc 100

Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
15 20 25

atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg 148

Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
30 35 40

gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac 196

Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
45 50 55 60

atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc 244

Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser
65 70 75

tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg 292
 Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu
 80 85 90
 gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg 340
 Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg
 95 100 105
 atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag 388
 Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln
 110 115 120
 cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa 436
 His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu
 125 130 135 140
 aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa 484
 Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln
 145 150 155
 gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc 532
 Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys
 160 165 170
 aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag 580
 Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys
 175 180 185
 ccg agg cgg tgagccgggc aggaggaagg agcctccctc agcgtttcgg 629
 Pro Arg Arg
 190
 gaaccagatc tctcaccagg 649

<210> 2
 <211> 191
 <212> PRT
 <213> Nucleotide Sequence of VEGF165

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 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 180 185 190

<210> 3

<211> 1094

<212> DNA

<213> Nucleotide Sequence of SOM175

<220>

<221> CDS

<222> (3)..(623)

<400> 3

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Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
 1 5 10 15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95

Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143

Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45

tggtaaaaaa cagccaagcc cccaagacct cagcccaggc agaagctgct ctaggacctg 803
 ggcctctcag agggctcttc tgccatccct tgtctccctg aggccatcat caaacaggac 863
 agagttggaa gaggagactg ggaggcagca agaggggtca cataccagct caggggagaa 923
 tggagtactg tctcagtttc taaccactct gtgcaagtaa gcattttaca actggctctt 983
 cctccctca ctaagaagac ccaaacctct gcataatggg atttgggctt tgggtacaaga 1043
 actgtgaccc ccaaccctga taaaagagat ggaaggaaaa aaaaaaaaaa a 1094

<210> 4
 <211> 207
 <212> PRT
 <213> Nucleotide Sequence of SOM175

<400> 4
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 1 5 10 15
 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
 130 135 140
 Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
 145 150 155 160
 Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala

165 170 175

His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
 180 185 190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 195 200 205

<210> 5
 <211> 993
 <212> DNA
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<220>
 <221> CDS
 <222> (3)..(566)

<400> 5
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Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
 1 5 10 15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95

Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143

Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191

Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 50 55 60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239

Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 65 70 75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287

Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80 85 90 95

caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg 335

Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
 100 105 110

ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
 Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
 115 120 125
 aaa aag gac agt gct gtg aag cca gat agc ccc agg ccc ctc tgc cca 431
 Lys Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro
 130 135 140
 cgc tgc acc cag cac cac cag cgc cct gac ccc cgg acc tgc cgc tgc 479
 Arg Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys
 145 150 155
 cgc tgc cga cgc cgc agc ttc ctc cgt tgc caa ggg cgg ggc tta gag 527
 Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu
 160 165 170 175
 ctc aac cca gac acc tgc agg tgc cgg aag ctg cga agg tgacacatgg 576
 Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
 180
 cttttcagac tcagcagggt gacttgcttc agaggctata tcccagtggg ggaacaaagg 636
 ggagcctgggt aaaaaacagc caagcccccagacctcagc ccaggcagaa gctgctctag 696
 gacctggggc tctcagaggg ctcttctgcc atcccttgtc tccctgaggg catcatcaaa 756
 caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata ccagctcagg 816
 ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat cttacaactg 876
 gctcttcttc cctcactaa gaagacccaa acctctgcat aatgggattt gggctttggg 936
 acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaaa aaaaaaa 993

<210> 6
 <211> 188
 <212> PRT
 <213> Nuc. Seq. of SOM175 Absent Exon 6

<400> 6
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
 1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95
Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
100 105 110
Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125
Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
130 135 140
Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
145 150 155 160
Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu Leu
165 170 175
Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg
180 185

<210> 7
<211> 858
<212> DNA
<213> Nuc. Seq. of SOM175 Absent Exons 6&7

<220>
<221> CDS
<222> (3)..(431)

<400> 7
cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag 47

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln
1 5 10 15

ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95

Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
20 25 30

cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
35 40 45

cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctg atg ggc acc 191
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
50 55 60

gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
65 70 75

ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
80 85 90 95

caa gtc cgg atg cag atc ctg atg atc cgg tac ccg agc agt cag ctg 335
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu
100 105 110

ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa 383
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys
115 120 125

aaa aag gac agt gct gtg aag cca gat agg tgc cgg aag ctg cga agg 431
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
130 135 140

tgacacatgg cttttcagac tcagcagggt gacttgccctc agaggctata tcccagtggg 491

ggaacaaagg ggagcctggg aaaaaacagc caagccccca agacctcagc ccaggcagaa 551

gctgctctag gacctgggcc tctcagaggg ctcttctgcc atcccttgtc tcctgagggc 611

catcatcaaa caggacagag ttggaagagg agactgggag gcagcaagag gggtcacata 671

ccagctcagg ggagaatgga gtactgtctc agtttctaac cactctgtgc aagtaagcat 731

cttacaactg gctcttccctc ccctcactaa gaagacccaa acctctgcat aatgggattt 791

gggctttggg acaagaactg tgacccccaa ccctgataaa agagatggaa ggaaaaaaaa 851

aaaaaaa

<210> 8
 <211> 143
 <212> PRT
 <213> Nuc. Seq. of SOM175 Absent Exons 6&7

<400> 8
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
 1 5 10 15
 Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30
 Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60
 Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Asp Ser Ala Val Lys Pro Asp Arg Cys Arg Lys Leu Arg Arg
 130 135 140

<210> 9
 <211> 910
 <212> DNA
 <213> Nuc. Seq. of SOM175 Absent Exon 4

<220>
 <221> CDS
 <222> (3)..(305)

<400> 9
 cc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag 47
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln 15
 1 5 10
 ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac 95

Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His
 20 25 30
 cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc 143
 Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys
 35 40 45
 cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc 191
 Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr
 50 55 60
 gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt 239
 Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly
 65 70 75
 ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac 287
 Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His
 80 85 90 95
 caa gtc cgg atg cag acc taaaaaaaaag gacagtgtg tgaagccaga 335
 Gln Val Arg Met Gln Thr
 100
 cagggctgcc actccccacc accgtcccca gcccgtttct gttccgggct gggactctgc 395
 ccccgagca cctccccag ctgacatcac ccatcccact ccagccccag gcccctctgc 455
 ccacgctgca cccagcacca ccagcgccct gacccccgga cctgccgctg ccgctgccga 515
 cgccgcagct tcttcggtg ccaagggcgg ggcttagagc tcaaccaga cacctgcagg 575
 tgccggaagc tgcgaagggtg acacatggct tttcagactc agcaggggtga cttgcctcag 635
 aggctatatc ccagtgggga acaaagagga gcttggtaaa aaacagccaa gcccccaaga 695
 cctcagccca ggcagaagct gctctaggac ctgggcctct cagagggctc ttctgccatc 755
 ccttgtctcc ctgaggccat catcaaacag gacagagttg gaagaggaga ctgggaggca 815
 gcaagagggg tcacatacca gctcagggga gaatggagta ctgtctcagt ttctaaccac 875

tctgtgcaag taagcatctt acaactggct cttcc

910

<210> 10
<211> 101
<212> PRT
<213> Nuc. Seq. of SOM175 Absent Exon 4

<400> 10
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95

Val Arg Met Gln Thr
100

<210> 11
<211> 42
<212> DNA
<213> Oligonucleotide

<400> 11
accaccacct ccctgggctg gcatgtggca cgtgcataaa cg

42

<210> 12
<211> 42
<212> DNA
<213> Oligonucleotide

<400> 12
agttgtttga ccacattgcc catgagttcc atgctcagag gc

42

<210> 13
<211> 38
<212> DNA

<213> Oligonucleotide

<400> 13
gatcctgggg ctggagtggg atggatgatg tcagctgg

38

<210> 14
<211> 40
<212> DNA
<213> Oligonucleotide

<400> 14
gcgggcagag gatcctgggg ctgtctggcc tcacagcact

40

<210> 15
<211> 236
<212> DNA
<213> Human SOM175

<400> 15
atgagggggc aggtacgtga ggtctccac agggccctgg aaagaatact tacatctgct 60
cccatgggtgt atgcaggtcc gagatgctga atacagatcc tcatgcaggt gtcaggcaac 120
ttttcaagac ctaaagacag gtgagtcttt ctctccgta ggctgcctcc agccccaggc 180
ccccactcc agccccagac ccagacacct gtagccctgc tcaggtgccg aggtga 236

<210> 16
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<212> DNA
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<220>
<221> CDS
<222> (166)..(789)

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gggggcccgc gagagccgc cccctgcgc ccgccccggg tccccgggtc cgcgccatgg 120
ggcggctctg gctgaccccc cccacaccg ccgggctagg gcccg atg agc ccc ctg 177
Met Ser Pro Leu
1
ctg cgt cgc ctg ctg ctt gtt gca ctg ctg cag ctg gct cgc acc cag 225

Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu Ala Arg Thr Gln
 5 10 15 20
 gcc cct gtg tcc cag ttt gat ggc ccc agt cac cag aag aaa gtg gtg 273
 Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln Lys Lys Val Val
 25 30 35
 cca tgg ata gac gtt tat gca cgt gcc aca tgc cag ccc agg gag gtg 321
 Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln Pro Arg Glu Val
 40 45 50
 gtg gtg cct ctg agc atg gaa ctc atg ggc aat gtg gtc aaa caa cta 369
 Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val Val Lys Gln Leu
 55 60 65
 gtg ccc agc tgt gtg act gtg cag cgc tgt ggt ggc tgc tgc cct gac 417
 Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys Cys Pro Asp
 70 75 80
 gat ggc ctg gaa tgt gtg ccc act ggg caa cac caa gtc cga atg cag 465
 Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val Arg Met Gln
 85 90 95 100
 atc ctc atg atc cag tac ccg agc agt cag ctg ggg gag atg tcc ctg 513
 Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly Glu Met Ser Leu
 105 110 115
 gga gaa cac agc caa tgt gaa tgc aga cct aaa aaa aag gag agt gct 561
 Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys Glu Ser Ala
 120 125 130
 gtg agg cca gac agg gtt gcc ata ccc cac cac cgt ccc cag ccc cgc 609
 Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg Pro Gln Pro Arg
 135 140 145
 tct gtt ccg ggc tgg gac tct acc ccg gga gca ccc tcc cca gct gac 657
 Ser Val Pro Gly Trp Asp Ser Thr Pro Gly Ala Pro Ser Pro Ala Asp
 150 155 160
 atc atc cat ccc act cca gcc cca gga tcc tct gcc cgc ctt gca ccc 705
 Ile Ile His Pro Thr Pro Ala Pro Gly Ser Ser Ala Arg Leu Ala Pro
 165 170 175 180
 agc gcc gcc aac gcc ctg acc ccc gga cct gcc gtt gcc gct gta gac 753
 Ser Ala Ala Asn Ala Leu Thr Pro Gly Pro Ala Val Ala Ala Val Asp

185

190

195

gcc gcc gct tcc tcc att gcc aag ggc ggg gct tag agctcaaccc 799

Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala
200 205

agacacctgt aggtgccgga agccgcgaaa gtgacaagct gctttccaga ctccacgggc 859

ccggctgctt ttatggccct gcttcacagg gagaagagtg gagcacaggc gtaacctcct 919

cagtctggga ggtcactgcc ccaggacctg gaccttttag agagctctct cgccatcttt 979

tatctcccag agctgccatc taacaattgt caaggaacct catgtctcac ctccaggggcc 1039

agggtactct ctcaactaac caccctgggc aagtgagcat cttctggctg gctgtctccc 1099

ctcactatga aaaccccaaa cttctaccaa taacgggatt tgggttctgt tatgataact 1159

gtgacacaca cacacactca cactctgata aaagagatgg agacactaaa aaaaaaaaaa 1219

aaaaaaaaaa aaaaaaaaaa aaa 1242

<210> 17

<211> 207

<212> PRT

<213> mVRF

<400> 17

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu
1 5 10 15
Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
20 25 30
Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
35 40 45
Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
50 55 60
Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80
Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
85 90 95
Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
100 105 110
Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125
Lys Glu Ser Ala Val Arg Pro Asp Arg Val Ala Ile Pro His His Arg
130 135 140

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Thr Pro Gly Ala Pro
 145 150 155 160
 Ser Pro Ala Asp Ile His Pro Thr Pro Ala Pro Gly Ser Ser Ala
 165 170 175
 Arg Leu Ala Pro Ser Ala Ala Asn Ala Leu Thr Pro Gly Pro Ala Val
 180 185 190
 Ala Ala Val Asp Ala Ala Ala Ser Ser Ile Ala Lys Gly Gly Ala
 195 200 205

<210> 18
 <211> 188
 <212> PRT
 <213> mVRF167

<400> 18
 Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Val Ala Leu Leu Gln Leu
 1 5 10 15
 Ala Arg Thr Gln Ala Pro Val Ser Gln Phe Asp Gly Pro Ser His Gln
 20 25 30
 Lys Lys Val Val Pro Trp Ile Asp Val Tyr Ala Arg Ala Thr Cys Gln
 35 40 45
 Pro Arg Glu Val Val Val Pro Leu Ser Met Glu Leu Met Gly Asn Val
 50 55 60
 Val Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln, Arg Cys Gly Gly
 65 70 75 80
 Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95
 Val Arg Met Gln Ile Leu Met Ile Gln Tyr Pro Ser Ser Gln Leu Gly
 100 105 110
 Glu Met Ser Leu Gly Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125
 Lys Glu Ser Ala Val Arg Pro Asp Ser Pro Arg Ile Leu Cys Pro Pro
 130 135 140
 Cys Thr Gln Arg Arg Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
 145 150 155 160
 Cys Arg Arg Arg Arg Phe Leu His Cys Gln Gly Arg Gly Leu Glu Leu
 165 170 175
 Asn Pro Asp Thr Cys Arg Cys Arg Lys Pro Arg Lys
 180 185

<210> 19
 <211> 188

<212> PRT
<213> hVRF167

<400> 19
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
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Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
20 25 30
Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
35 40 45
Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
50 55 60
Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
65 70 75 80
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Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
115 120 125
Lys Asp Ser Ala Val Lys Pro Asp Ser Pro Arg Pro Leu Cys Pro Arg
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Cys Thr Gln His His Gln Arg Pro Asp Pro Arg Thr Cys Arg Cys Arg
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Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met
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Ser Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
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